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Sequence Listing was accepted.
See attached Validation Report.
If you need help call the Patent Electronic Business Center at (866) 217-9197 (toll free).
Reviewer: Durreshwar Anjum
Timestamp: [year=2010; month=5; day=3; hr=10; min=10; sec=43; ms=829;]
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Validated By CRFValidator v 1.0.3

Application No: 10590870 Version No: 1.0

Input Set:

Output Set:

Started: 2010-04-23 14:53:05.942
Finished: 2010-04-23 14:53:09.612
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 670 ms
Total Warnings: 51
Total Errors: 2
No. of SeqIDs Defined: 51
Actual SeqID Count: 51

Error code		Error Description
W	213	Artificial or Unknown found in <213> in SEQ ID (1)
E	355	Empty lines found between the amino acid numbering and the
E	321	No. of Bases conflict, this line has no nucleotides SEQID (1)
W	213	Artificial or Unknown found in <213> in SEQ ID (2)
W	213	Artificial or Unknown found in <213> in SEQ ID (3)
W	213	Artificial or Unknown found in <213> in SEQ ID (4)
W	213	Artificial or Unknown found in <213> in SEQ ID (5)
W	213	Artificial or Unknown found in <213> in SEQ ID (6)
W	213	Artificial or Unknown found in <213> in SEQ ID (7)
W	213	Artificial or Unknown found in <213> in SEQ ID (8)
W	213	Artificial or Unknown found in <213> in SEQ ID (9)
W	213	Artificial or Unknown found in <213> in SEQ ID (10)
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W	213	Artificial or Unknown found in <213> in SEQ ID (12)
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Input Set:

Output Set:

Started: 2010-04-23 14:53:05.942
Finished: 2010-04-23 14:53:09.612
Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 670 ms
Total Warnings: 51
Total Errors: 2
No. of SeqIDs Defined: 51
Actual SeqID Count: 51

Error code	Error Description
W 213	Artificial or Unknown found in <213> in SEQ ID (19)
W 213	Artificial or Unknown found in <213> in SEQ ID (20) This error has occured more than 20 times, will not be displayed

SEQUENCE LISTING

<110> Fox, Judith A.
Harding, Fiona A.
Rashid, M. Harunur
Schellenberger, Volker

<120> CAB Molecules

<130> GC839-US

<140> 10590870
<141> 2010-04-23

<150> PCT/US05/12270
<151> 2005-04-12

<150> US 60/562,386
<151> 2004-04-15

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<151> 2004-12-14

<160> 51

<170> PatentIn version 3.2

<210> 1
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<212> PRT
<213> Artificial Sequence

<220>
<223> engineered T84.66 antibody

<400> 1

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Gln Arg Ala Thr Met Ser Cys Arg Ala Gly Glu Ser Val Asp Ile Phe
            20                  25                  30
Gly Val Gly Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45
Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Val
    50                  55                  60
Arg Phe Ser Gly Thr Gly Ser Arg Thr Asp Phe Thr Leu Ile Ile Asp
65                  70                  75                  80
Pro Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Thr Asn
                85                  90                  95
Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
            100                 105                 110
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly

        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
    130                 135                 140
Leu Gln Gln Ser Gly Ala Glu Leu Val Glu Pro Gly Ala Ser Val Lys
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145                 150                 155                 160
Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Met His
                165                 170                 175
Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly Arg Ile
            180                 185                 190
Asp Pro Ala Asn Gly Asn Ser Lys Tyr Val Pro Lys Phe Gln Gly Lys
        195                 200                 205
Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr Leu Gln Leu
    210                 215                 220
Thr Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Pro Phe
225                 230                 235                 240
Gly Tyr Tyr Val Ser Asp Tyr Ala Met Ala Tyr Trp Gly Gln Gly Thr
                245                 250                 255
Ser Val Thr Val Ser Ser
            260
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<210> 2
<211> 623
<212> PRT
<213> Artificial Sequence

<220>
<223> CAB 1.10 construct

<400> 2

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1               5                   10                  15
Gln Arg Ala Thr Met Ser Cys Arg Ala Gly Glu Ser Val Asp Ile Phe
            20                  25                  30
Gly Val Gly Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45
Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Val
    50                  55                  60
Arg Phe Ser Gly Thr Gly Ser Arg Thr Asp Phe Thr Leu Ile Ile Asp
65                  70                  75                  80
Pro Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Thr Asn
                85                  90                  95
Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
            100                 105                 110
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
    130                 135                 140
Leu Gln Gln Ser Gly Ala Glu Leu Val Glu Pro Gly Ala Ser Val Lys
145                 150                 155                 160
Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Met His
                165                 170                 175
Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly Arg Ile
            180                 185                 190
Asp Pro Ala Asn Gly Asn Ser Lys Tyr Val Pro Lys Phe Gln Gly Lys
        195                 200                 205
Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr Leu Gln Leu
    210                 215                 220
Thr Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Pro Phe
225                 230                 235                 240
Gly Tyr Tyr Val Ser Asp Tyr Ala Met Ala Tyr Trp Gly Gln Gly Thr
                245                 250                 255
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Ser Val Thr Val Ser Ser Thr Pro Val Ser Glu Lys Gln Leu Ala Glu
            260                 265                 270
Val Val Ala Asn Thr Ile Thr Pro Leu Met Lys Ala Gln Ser Val Pro
        275                 280                 285
Gly Met Ala Val Ala Val Ile Tyr Gln Gly Lys Pro His Tyr Tyr Thr
    290                 295                 300
Phe Gly Lys Ala Asp Ile Ala Ala Asn Lys Pro Val Thr Pro Gln Thr
305                 310                 315                 320
Leu Phe Glu Leu Gly Ser Ile Ser Lys Thr Phe Thr Gly Val Leu Gly
                325                 330                 335
Gly Asp Ala Ile Ala Arg Gly Glu Ile Ser Leu Asp Asp Ala Val Thr
            340                 345                 350
Arg Tyr Trp Pro Gln Leu Thr Gly Lys Gln Trp Gln Gly Ile Arg Met
        355                 360                 365
Leu Asp Leu Ala Thr Tyr Thr Ala Gly Gly Leu Pro Leu Gln Val Pro
    370                 375                 380
Asp Glu Val Thr Asp Asn Ala Ser Leu Leu Arg Phe Tyr Gln Asn Trp
385                 390                 395                 400
Gln Pro Gln Trp Lys Pro Gly Thr Thr Arg Leu Tyr Ala Asn Ala Ser
                405                 410                 415
Ile Gly Leu Phe Gly Ala Leu Ala Val Lys Pro Ser Gly Met Pro Tyr
            420                 425                 430
Glu Gln Ala Met Thr Thr Arg Val Leu Lys Pro Leu Lys Leu Asp His
        435                 440                 445
Thr Trp Ile Asn Val Pro Lys Ala Glu Glu Ala His Tyr Ala Trp Gly
    450                 455                 460
Tyr Arg Asp Gly Lys Ala Val Arg Val Ser Pro Gly Met Leu Asp Ala
465                 470                 475                 480
Gln Ala Tyr Gly Val Lys Thr Asn Val Gln Asp Met Ala Asn Trp Val
                485                 490                 495
Met Ala Asn Met Ala Pro Glu Asn Val Ala Asp Ala Ser Leu Lys Gln
            500                 505                 510
Gly Ile Ala Leu Ala Gln Ser Arg Tyr Trp Arg Ile Gly Ser Met Tyr
        515                 520                 525
Gln Gly Leu Gly Trp Glu Met Leu Asn Trp Pro Val Glu Ala Asn Thr
    530                 535                 540
Val Val Glu Thr Ser Phe Gly Asn Val Ala Leu Ala Pro Leu Pro Val
545                 550                 555                 560
Ala Glu Val Asn Pro Pro Ala Pro Pro Val Lys Ala Ser Trp Val His
                565                 570                 575
Lys Thr Gly Ser Thr Gly Gly Phe Gly Ser Tyr Val Ala Phe Ile Pro
            580                 585                 590
Glu Lys Gln Ile Gly Ile Val Met Leu Ala Asn Thr Ser Tyr Pro Asn
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    610                 615                 620
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<210> 3
<211> 786
<212> DNA

<213> Artificial Sequence

<220>
<223> engineered T84.66 antibody

<400> 3

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caacagaaac cgggtcagcc gccaaaactg ctgatctatc gtgcttctaa cctggagtcc 180
ggcatcccgg tacgtttctc cggtactggc tctcgtactg attttaccct gattatcgac 240
ccggtggaag cagacgatgt tgccacctac tattgccagc agaccaacga ggatccgtac 300
accttcggtg gcggtactaa actggagatc aaaggcggtg gtggttctgg tggtggtggt 360
agcggcggcg gtggtagcgg tggcggtggc agcggtggtg gtggctctgg tggcggtggc 420
tctgaagtgc agctgcagca gtccggtgcg gagctcgttg aaccgggcgc ttctgtgaaa 480
ctgtcttgca ctgcatctgg tttcaacatt aaggacacct acatgcactg ggtgaaacaa 540
cgcccggaac agggtctgga gtggatcggt cgcatcgatc cggctaacgg taacagcaaa 600
tacgtgccaa aattccaggg taaagcaacc atcactgctg atacctcctc taacactgct 660
tacctgcagc tgacttccct gactagcgaa gacaccgcgg tttattactg cgctccgttc 720
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<210> 4
<211> 1869
<212> DNA
<213> Artificial Sequence

<220>
<223> CAB 1.10 construct

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caacagaaac cgggtcagcc gccaaaactg ctgatctatc gtgcttctaa cctggagtcc 180
ggcatcccgg tacgtttctc cggtactggc tctcgtactg attttaccct gattatcgac 240
ccggtggaag cagacgatgt tgccacctac tattgccagc agaccaacga ggatccgtac 300
accttcggtg gcggtactaa actggagatc aaaggcggtg gtggttctgg tggtggtggt 360
agcggcggcg gtggtagcgg tggcggtggc agcggtggtg gtggctctgg tggcggtggc 420
tctgaagtgc agctgcagca gtccggtgcg gagctcgttg aaccgggcgc ttctgtgaaa 480
ctgtcttgca ctgcatctgg tttcaacatt aaggacacct acatgcactg ggtgaaacaa 540
cgcccggaac agggtctgga gtggatcggt cgcatcgatc cggctaacgg taacagcaaa 600
tacgtgccaa aattccaggg taaagcaacc atcactgctg atacctcctc taacactgct 660
tacctgcagc tgacttccct gactagcgaa gacaccgcgg tttattactg cgctccgttc 720
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cactattaca catttggcaa ggccgatatc gcggcgaata aacccgttac gcctcagacc 960
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aagcagtggc agggtattcg tatgctggat ctcgccacct acaccgctgg cggcctgccg 1140
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cagccgcagt ggaagcctgg cacaacgcgt ctttacgcca acgccagcat cggtcttttt 1260
ggtgcgctgg cggtcaaacc ttctggcatg ccctatgagc aggccatgac gacgcgggtc 1320
cttaagccgc tcaagctgga ccatacctgg attaacgtgc cgaaagcgga agaggcgcat 1380
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gcgccggaga acgttgctga tgcctcactt aagcagggca tcgcgctggc gcagtcgcgc 1560
tactggcgta tcgggtcaat gtatcagggt ctgggctggg agatgctcaa ctggcccgtg 1620
gaggccaaca cggtggtcga gacgagtttt ggtaatgtag cactggcgcc gttgcccgtg 1680
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<210> 5
<211> 262
<212> PRT
<213> Artificial Sequence

<220>
<223> CAB 1.11 construct

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35 40 45
Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Val
50 55 60
Arg Phe Ser Gly Thr Gly Ser Gly Thr Asp Phe Thr Leu Ile Ile Asp
65 70 75 80
Pro Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Thr Asn
85 90 95
Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
100 105 110
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
115 120 125
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
130 135 140
Leu Gln Gln Ser Gly Ala Glu Leu Val Glu Pro Gly Ala Ser Val Lys
145 150 155 160
Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Met His
165 170 175
Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly Arg Ile
180 185 190
Asp Pro Ala Asn Gly Asn Ser Lys Tyr Val Pro Lys Phe Gln Gly Lys
195 200 205
Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr Leu Gln Leu
210 215 220
Thr Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Pro Phe
225 230 235 240
Gly Tyr Tyr Val Ser Asp Tyr Ala Met Ala Tyr Trp Gly Gln Gly Thr
245 250 255
Ser Val Thr Val Ser Ser
260

<210> 6
<211> 786
<212> DNA
<213> Artificial Sequence

<220>
<223> CAB 1.11 construct

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caacagaaac cgggtcagcc gccaaaactg ctgatctatc gtgcttctaa cctggagtcc 180
ggcatcccgg tacgtttctc cggtactggc tctggtactg attttaccct gattatcgac 240

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ccggtggaag cagacgatgt tgccacctac tattgccagc agaccaacga ggatccgtac    300
accttcggtg gcggtactaa actggagatc aaaggcggtg gtggttctgg tggtggtggt    360
agcggtggcg gtggtagcgg tggcggtggc agcggtggtg gtggctctgg tggcggtggc    420
tctgaagtgc agctgcagca gtccggtgcg gagctcgttg aaccgggcgc ttctgtgaaa    480
ctgtcttgca ctgcatctgg tttcaacatt aaggacacct acatgcactg ggtgaaacaa    540
cgcccggaac agggtctgga gtggatcggt cgcatcgatc cggctaacgg taacagcaaa    600
tacgtgccaa aattccaggg taaagcaacc atcactgctg atacctcctc taacactgct    660
tacctgcagc tgacttccct gactagcgaa gacaccgcgg tttattactg cgctccgttc    720
ggctactatg tcagcgatta cgcaatggcc tactggggtc agggcacctc tgttaccgtt    780
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<210> 7
<211> 623
<212> PRT
<213> Artificial Sequence

<220>
<223> CAB 1.11 construct

<400> 7

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            20                  25                  30
Gly Val Gly Phe Leu His Trp Tyr Gln Gln Lys Pro Gly Gln Pro Pro
        35                  40                  45
Lys Leu Leu Ile Tyr Arg Ala Ser Asn Leu Glu Ser Gly Ile Pro Val
    50                  55                  60
Arg Phe Ser Gly Thr Gly Ser Gly Thr Asp Phe Thr Leu Ile Ile Asp
65                  70                  75                  80
Pro Val Glu Ala Asp Asp Val Ala Thr Tyr Tyr Cys Gln Gln Thr Asn
                85                  90                  95
Glu Asp Pro Tyr Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys Gly
            100                 105                 110
Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly
        115                 120                 125
Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Gly Ser Glu Val Gln
    130                 135                 140
Leu Gln Gln Ser Gly Ala Glu Leu Val Glu Pro Gly Ala Ser Val Lys
145                 150                 155                 160
Leu Ser Cys Thr Ala Ser Gly Phe Asn Ile Lys Asp Thr Tyr Met His
                165                 170                 175
Trp Val Lys Gln Arg Pro Glu Gln Gly Leu Glu Trp Ile Gly Arg Ile
            180                 185                 190
Asp Pro Ala Asn Gly Asn Ser Lys Tyr Val Pro Lys Phe Gln Gly Lys
        195                 200                 205
Ala Thr Ile Thr Ala Asp Thr Ser Ser Asn Thr Ala Tyr Leu Gln Leu
    210                 215                 220
Thr Ser Leu Thr Ser Glu Asp Thr Ala Val Tyr Tyr Cys Ala Pro Phe
225                 230                 235                 240
Gly Tyr Tyr Val Ser Asp Tyr Ala Met Ala Tyr Trp Gly Gln Gly Thr
                245                 250                 255
Ser Val Thr Val Ser Ser Thr Pro Val Ser Glu Lys Gln Leu Ala Glu
            260                 265                 270
Val Val Ala Asn Thr Ile Thr Pro Leu Met Lys Ala Gln Ser Val Pro
        275                 280                 285
Gly Met Ala Val Ala Val Ile Tyr Gln Gly Lys Pro His Tyr Tyr Thr
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    290                 295                 300
Phe Gly Lys Ala Asp Ile Ala Ala Asn Lys Pro Val Thr Pro Gln Thr
305                 310                 315                 320
Leu Phe Glu Leu Gly Ser Ile Ser Lys Thr Phe Thr Gly Val L
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